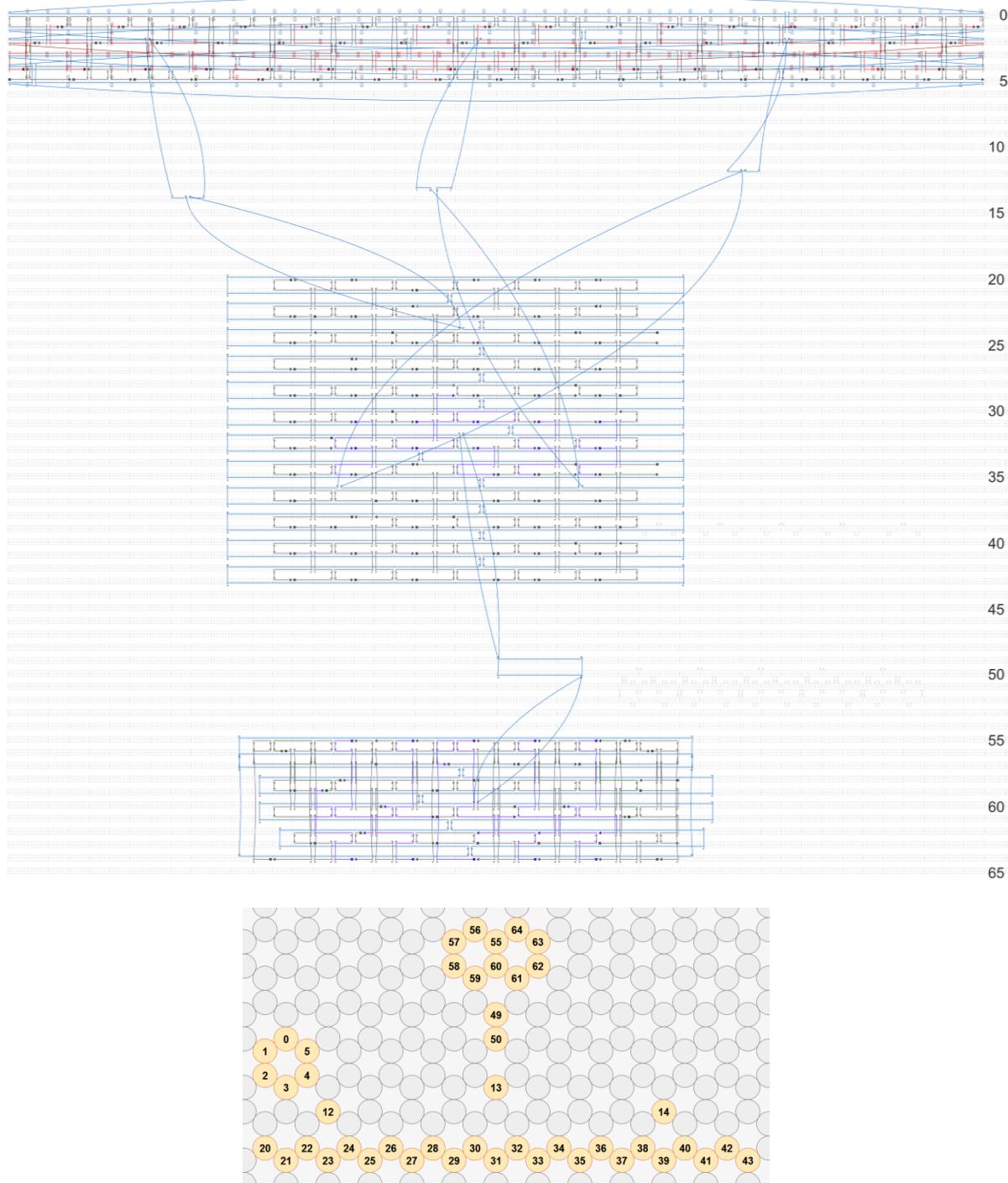


Supplementary Information for

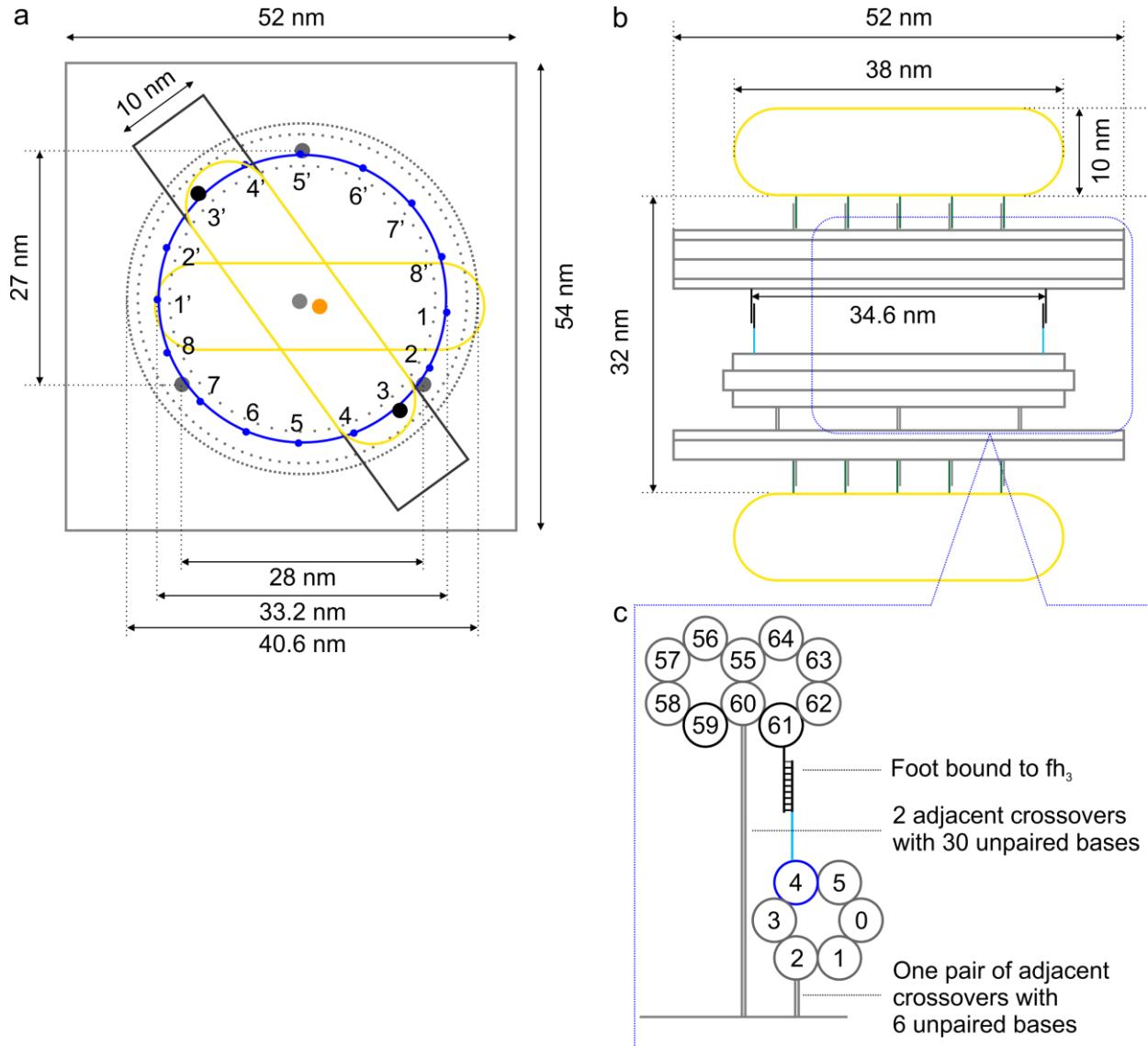
A rotary plasmonic nanoclock

Xin et al.

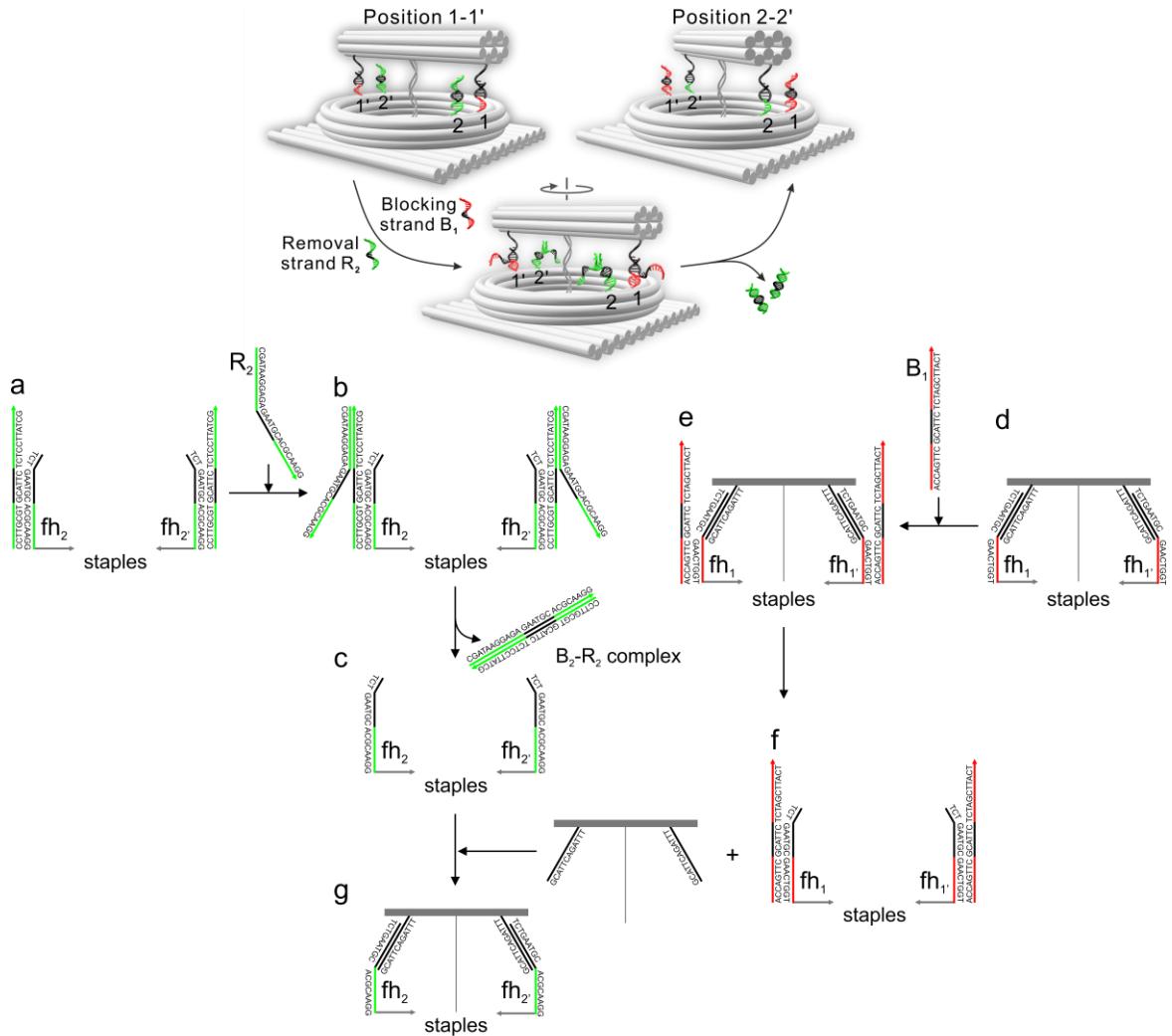
Correspondence to: na.liu@kip.uni-heidelberg.de



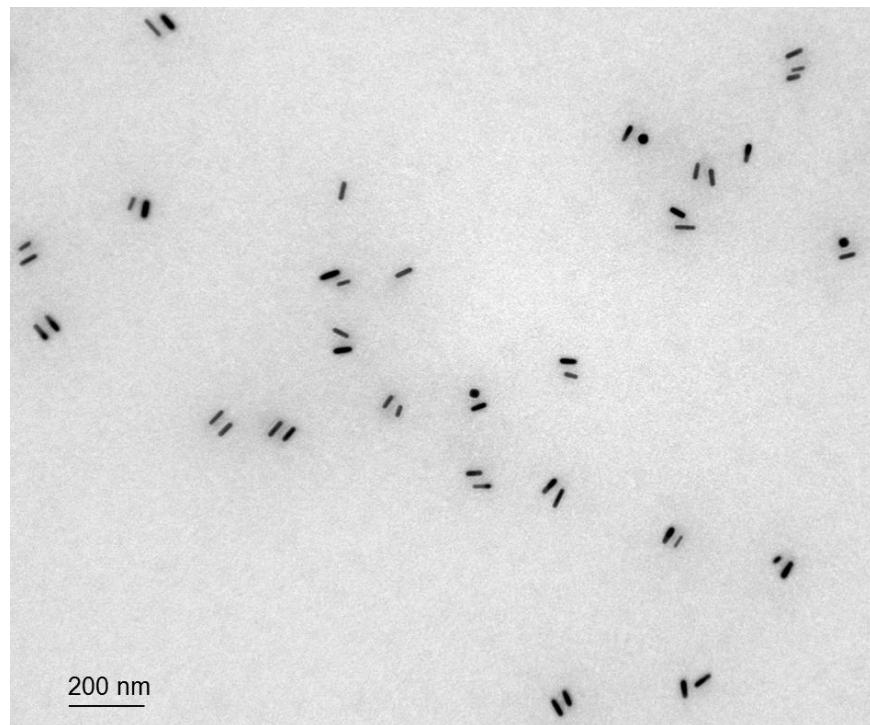
Supplementary Figure 1 | Strand routing diagram of the DNA origami structure for the stepwise plasmonic nanoclock. Staples for two foot strands (green), 16 footholds (red), 20 capture strands (violet).



Supplementary Figure 2 | Structural details of the stepwise plasmonic nanoclock. **a**, Top and **b**, Side views of the plasmonic nanoclock at position 3-3'. Three grey dots under the blue ring in the top view represent the positions of the three pairs of adjacent crossovers with 6 unpaired bases to connect the lower surface of the 6-helix ring and the upper surface of the single-layer plate. The grey dot in the center of the circle represents the position of 2 adjacent scaffold crossovers with 30 unpaired bases used to connect the centers of the 10-helix bundle and the single-layer plate, which are not shown in the side view. The orange dot is the center of the capturing strands extended from the bottom of the plate for attaching the stator AuNR. The orange dot and grey dot don't coincide with each other (the lateral distance between them is ~2.3 nm), meaning the two AuNRs are not coaxial. The four circles in the top view represent the positions of the different helices in the ring. The crossovers used to immobilize the ring on the plate are distributed on helix 2 and the footholds are extended from helix 4. Both helices are along the blue circle in the top view. The origami bundle is about 10 nm in width and 52 nm in length. The two black dots along the diagonal direction of the rotor represent the two feet and coincide with the two small blue dots at position 3-3', meaning the two feet are bound to fh_3 and $fh_{3'}$, respectively. The rotor is fixed at position 3-3'. **c**, Enlarged view of connections between ring track, rotor and plate. Scaffold crossovers are used to immobilize the rotor and ring track on the plate. Meanwhile, the rotor and ring track are linked via foot-foothold interaction.



Supplementary Figure 3 | Schematic illustration of the stepwise rotation from position 1-1' to position 2-2'. Each pair of the colored foothold strands on the ring track has a specific sequence. The two feet at the ends of the DNA bundle interact with a given pair of the footholds to determine the rotor position. For example, at the initial state the rotor is fixed at position 1-1'. At this state, the feet are bound to the red foothold pair (fh₁ and fh_{1'}) and all other footholds are blocked. (a-c) R₂ is first added to activate position 2-2'. B₂ is dissociated by R₂ through branch migration, triggered by top domain of B₂, and the green pair of the footholds (fh₂ and fh_{2'}) is activated. (d-f) Next, B₁ is added to block position 1-1'. Fh₁ and fh_{1'} are deactivated by B₁ mediated through toehold domains on fh₁ and fh_{1'}. (g) Two feet are free for capturing fh₂ and fh_{2'} and driving the rotor to position 2-2'. As a result, one step of the clockwise rotation is accomplished.



Supplementary Figure 4 | TEM image of the stepwise plasmonic nanoclocks at position 1-1'.

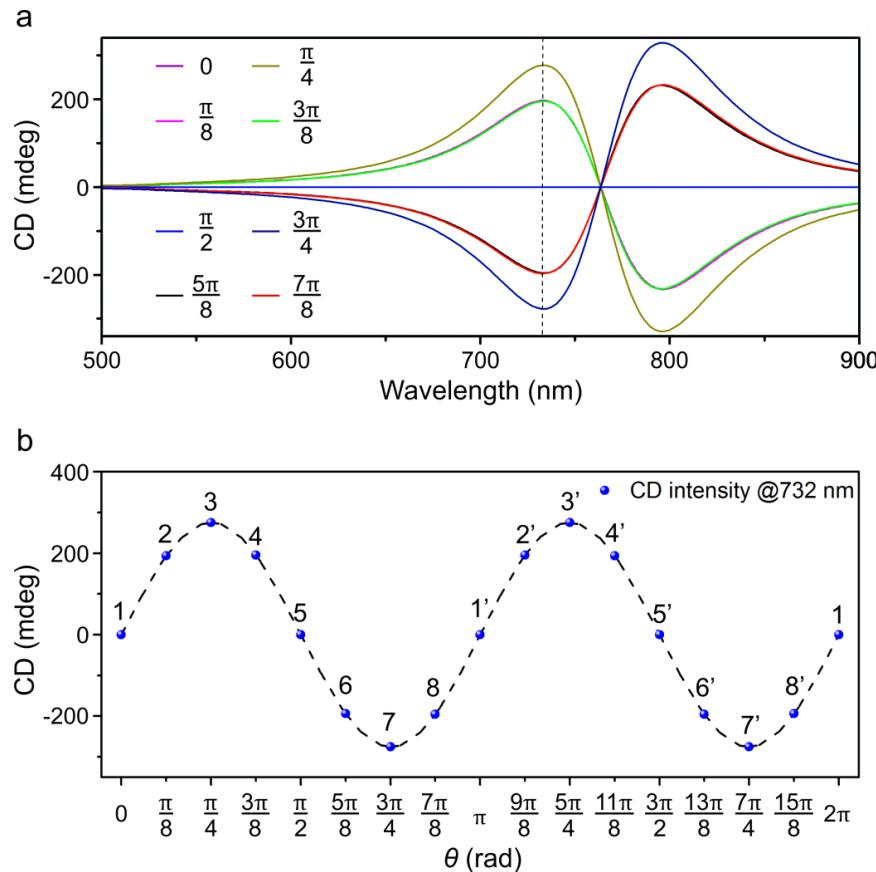
Theoretical calculations were performed using commercial software COMSOL Multiphysics based on a finite element method. The origin of the bisignate CD is a consequence of Coulomb interaction between the dipoles of the two AuNRs. The CD signal was calculated as a difference in extinction for the left- and right-circularly polarized light. Since the plasmonic assemblies were dispersed in a solution, we carried out orientational averaging. Averaging over all possible orientations at defined light incidence is equivalent to averaging over all incident directions of light for a nanostructure with defined orientation. It has been demonstrated both analytically and numerically that averaging over six orthogonal directions of light incidence is sufficient to give accurate CD. In order to account for the inhomogeneous broadening due to the polydispersity of the AuNRs, the experimental dielectric function of Au was modified by including an additional term:

$$\varepsilon_{\text{effective}}(\omega) = \varepsilon_{\text{bulk}}(\omega) + \varepsilon_{\text{correction}}(\omega) \quad (1)$$

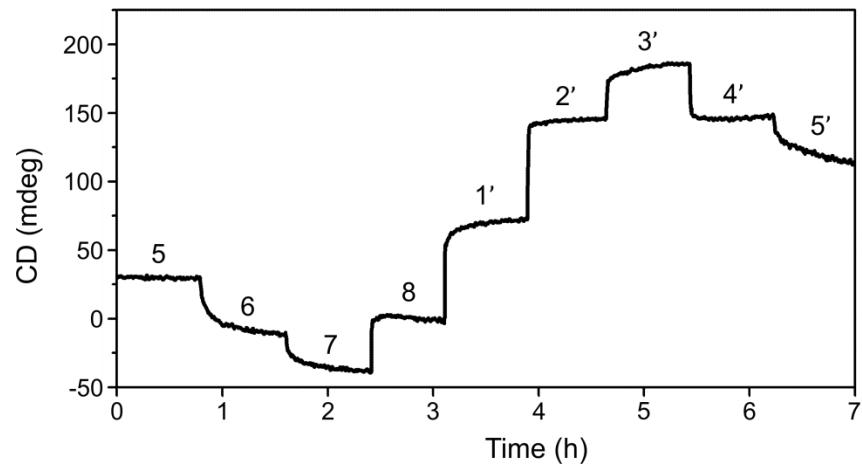
where the dielectric function of bulk Au, $\varepsilon_{\text{bulk}}$ is from the Johnson and Christy values, and the correction term is introduced following a standard approach:

$$\varepsilon_{\text{correction}}(\omega) = \frac{\omega_p^2}{\omega^2 + i\omega\gamma} - \frac{\omega_p^2}{\omega^2 + i\omega\Gamma_{\text{broad}}} \quad (2)$$

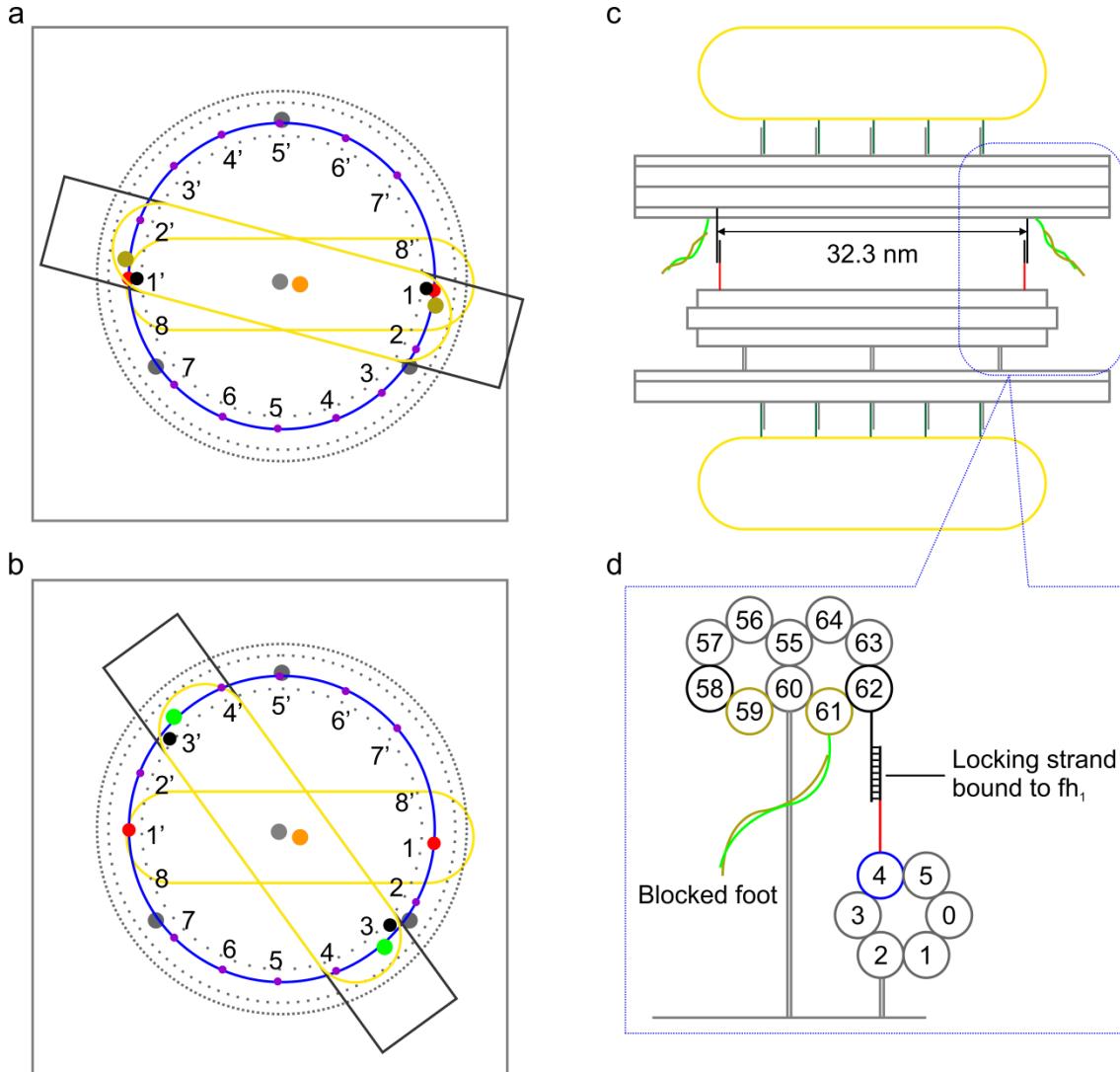
$\omega_p = 8.754$ eV and $\gamma = 0.0724$ eV are the Drude parameters, respectively. Γ_{broad} is 0.362 eV.



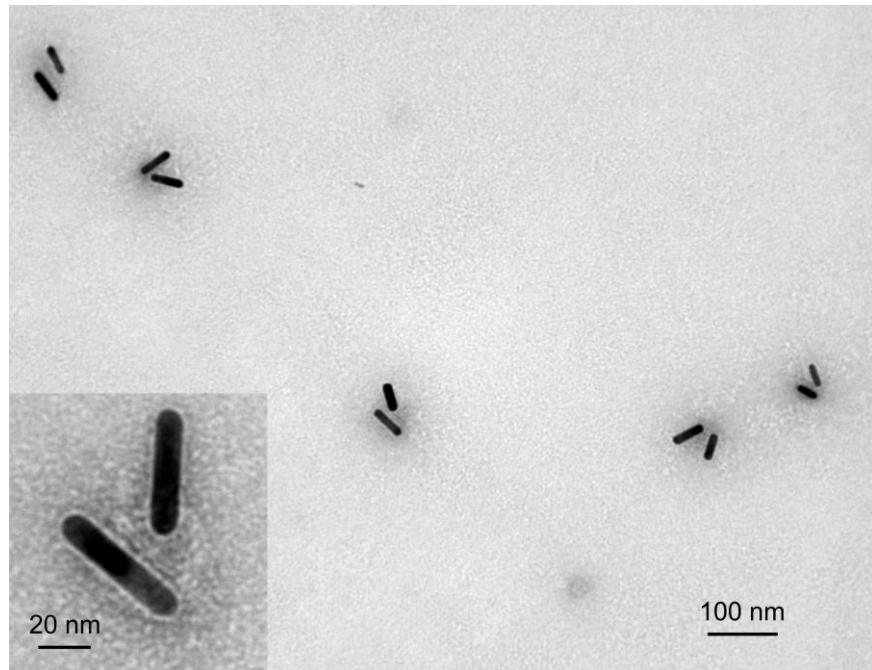
Supplementary Figure 5 | Theoretical results for the 16 states of the plasmonic nanoclock. **a**, Calculated CD spectra at different rotation angles. **b**, CD intensity at 732 nm as a function of the rotation angle θ .



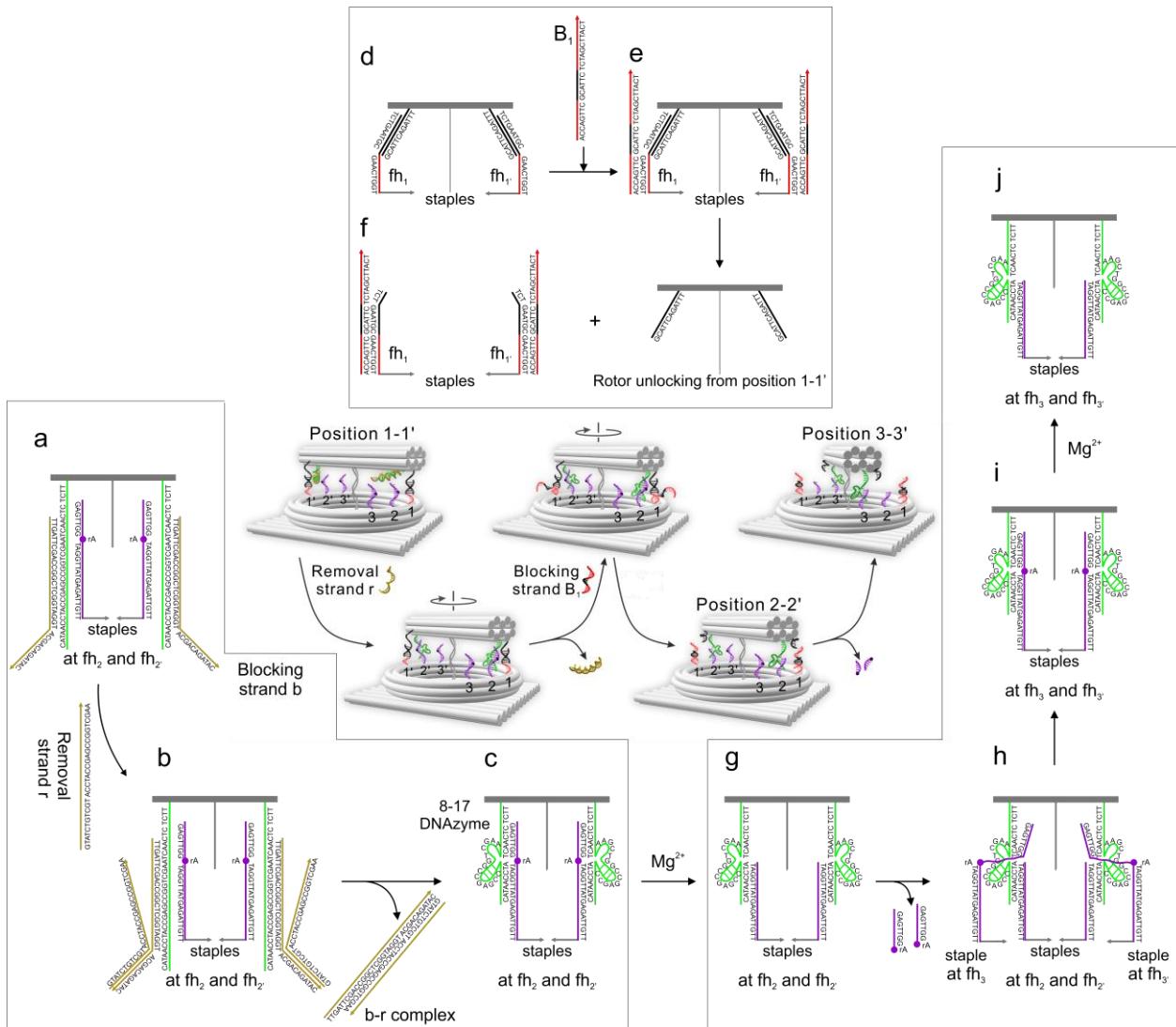
Supplementary Figure 6 | Kinetics of the stepwise rotations driven by corresponding DNA fuels. The concentration of the AuNRs is about 1.2 nM. This result also indicates that the plasmonic nanoclock can perform stepwise rotations from any starting position.



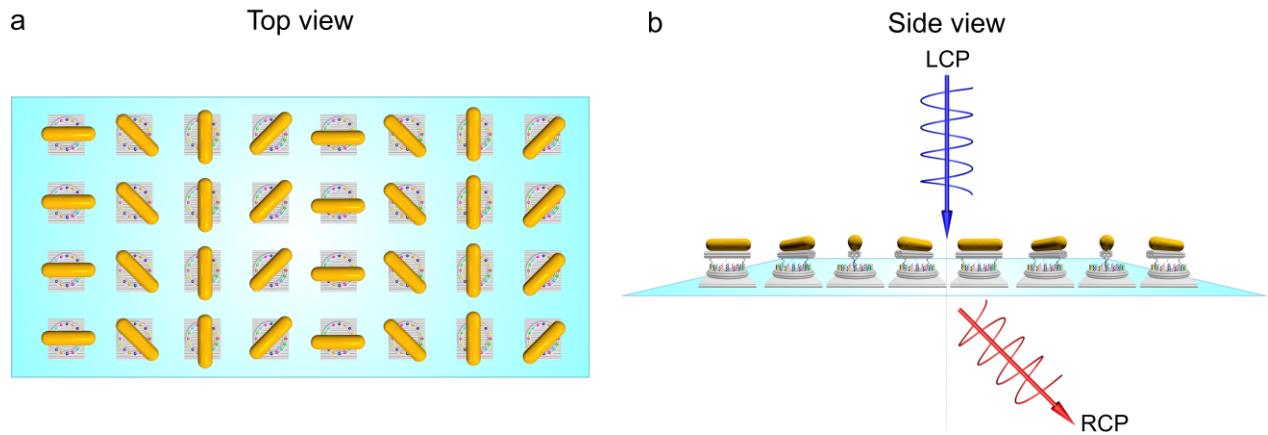
Supplementary Figure 7 | Structural details of the autonomous plasmonic nanoclock. Top-view of the plasmonic nanoclock with track arrangement of 1–2–3–4–5–6–7 at **a**, position 1–1' and **b**, position 3–3'. Substrates (purple dots) as footholds are arranged on helix 4 (blue circle). fh_1 and $\text{fh}_{1'}$ are working as lower locking strands (red dots). **a**, Two brown dots along the diagonal direction of the rotor represent that the DNAzyme feet are blocked. Two black dots next to the blocked feet represent the upper locking strands. They coincide with the red dots, which means the rotor is fixed at position 1–1' through hybridization between the upper and lower locking strands. **b**, Two green dots represent the positions of the two activated feet superimposed with the two small purple dots at position 3–3'. The feet are bound to the substrates at fh_3 and $\text{fh}_{3'}$, and the rotor is fixed at position 3–3'. **c**, Side-view of the plasmonic nanoclock with track arrangement of 1–2–3–4–5–6–7 at position 1–1' and the feet are blocked. The distance between the two upper locking strands is about 32.3 nm. **d**, Enlarged view of connection between ring track and rotor by the locking strands on helix 62 and 4. The foot strand (green) on helix 61 is blocked by blocking strand b (brown).



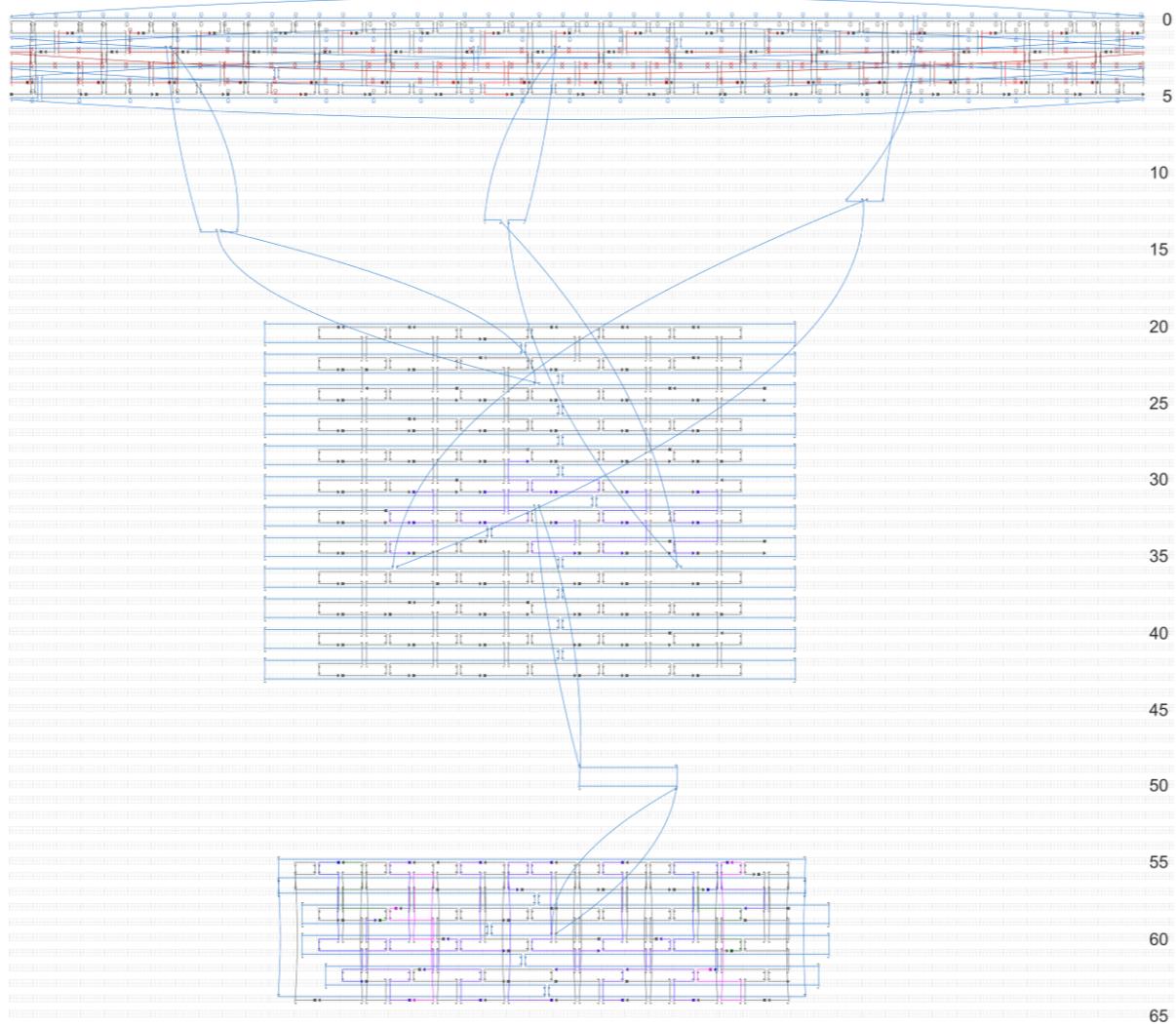
Supplementary Figure 8 | TEM image of the autonomous plasmonic nanoclocks at position 1-1'.



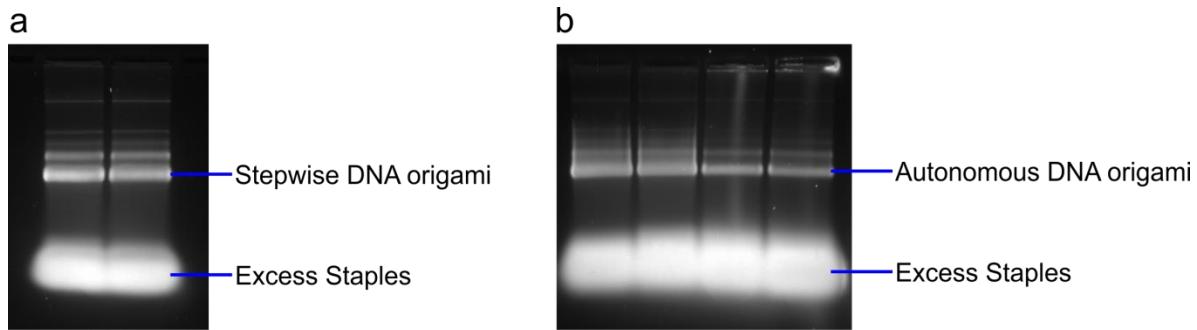
Supplementary Figure 9 | Schematic illustration of the autonomous rotation from position 1-1' to position 3-3'. Before rotation, feet (green) are blocked by blocking strand b (brown). Each substrate (purple strand) contains a ribonucleotide (purple dot) in sequence at the 8 base from 5' end. Two upper locking strands (black) next to feet hybridize with fh_1 and fh_1' to fix the rotor at position 1-1'. The autonomous rotation is actuated through two sets of toehold-mediated strand displacement reactions. (a-c) Addition of removal strand r (brown), the feet are activated to interact with substrates at fh_2 and fh_2' . (d-f) B_1 is added to break the interactions between the locking strands and free the rotor for autonomous rotation. (g-j) In the presence of Mg^{2+} , the 8-17 DNAzyme in the foot strands catalyze the hydrolysis of the substrate at the RNA base (rA). The substrates are cut into two short segments (8-nt free segment and 17-nt staple extension). As the free segments diffuse in the solution, the adjacent pair of the intact substrates at fh_3 and fh_3' are able to interact with the foot strands. Subsequently, the feet will move forward to position 3-3'. The processive rotation is therefore based on the burnt-bridge mechanism.



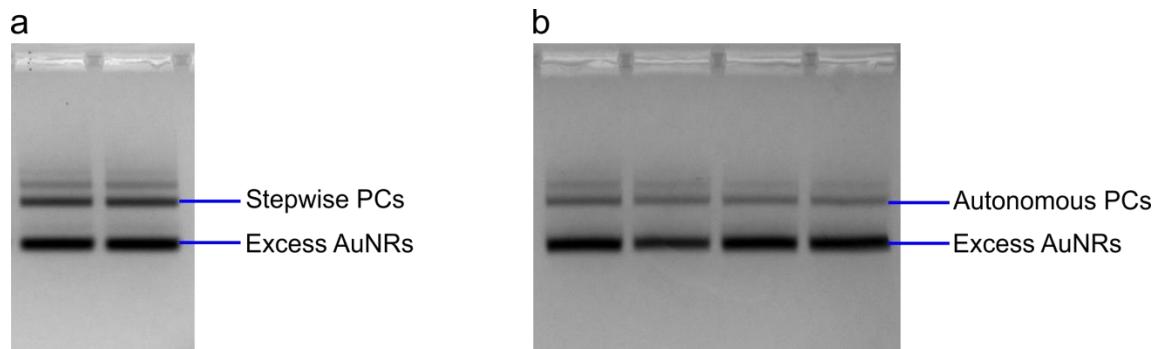
Supplementary Figure 10 | Visionary scheme of a dynamic optical metasurface, on which the DNA-assembled rotary AuNRs work as individual plasmonic pixels to dynamically shape the wavefront of light. The orientations of these AuNRs could be independently controlled by DNA nanotechnology. For instance, with a linear phase gradient distribution (a), anomalous refraction by the metasurface (b) could be achieved.



Supplementary Figure 11 | Strand routing diagram of the DNA origami structure for the autonomous plasmonic nanoclock. Staples for two foot strands (green), two upper locking strands (magenta), 16 footholds (positions for lower locking strands and substrates, red) and 20 capture strands (violet). Two blue strands represent the staples revised in the autonomous design.



Supplementary Figure 12 | Characterization and purification of the DNA origami structures by agarose gel electrophoresis. **a**, DNA origami for assembly of the stepwise plasmonic nanoclocks. **b**, DNA origami for assembly of the autonomous plasmonic nanoclocks.



Supplementary Figure 13 | Characterization and purification of the plasmonic nanoclocks by agarose gel electrophoresis. **a**, Stepwise plasmonic nanoclocks. **b**, Autonomous plasmonic nanoclocks. PCs: plasmonic nanoclocks

Supplementary Table 1 | Sequences of the stepwise plasmonic nanoclocks.

Unmodified staples	Sequence (5'-3')
2[135]	CAAGAGAATCGATGAAGTTA
1[270]	ATTCTTACCACTATAAAGACC
57[151]	CCAGACGTCGGTGGTGCGGTTCT
35[99]	AATAAAGGAACCCATGTACCGAACGCCT
41[119]	TCACCCTAGGAAGTTCCATTACTCATC
39[98]	GTTGAAACCATGCCAACGCAGGAGTTA
41[203]	CTTGACAGGAACCGAACTGACAAATCCG
43[182]	GATAAATTGTGTCGCAACTTTCATCAA
37[203]	CACATTGGAGAAAAATCTATCATTG
37[140]	AAAGTTTCTGTATGGATTCTTTAA
37[98]	GTAGCATGAGTGAGAATAGAATTTCAC
29[140]	GTAAAACGCCACGGAACGGCAGAAC
27[119]	ATCGCACCTGTTGGGAGGGCACGCCAG
39[140]	TTGTATCTAACAGCTTGATAGAAAGAC
27[203]	AAATACAAACCGAGGAAACGCTCTTACC
39[182]	TAATTCGACGAGAACACCAAGGCTGG
41[140]	AGCATCGAGGACTAAAGACTTATTATAC
29[182]	AATAGCACACAAGAATTGAGTGAGAATA
35[182]	ATTACCGCTCATCGAGAACAAAGATTCA
26[118]	TGGGATAGGTACGTTCGCGTAAATTCA
23[98]	AAGAGAACGATTAATTTGCCATCA
31[98]	GTGGTATAAAAGTTGAGTAAGAAGGA
25[98]	AAAATAATTGGTAGATGGGGACGAC
27[182]	CAGTATGACGGAATACCCAAAACAATGA
25[140]	ACATTAAGTGGAACAAACGGAGCTTC
37[182]	TCAGTTGAAAACGAACTAACGATGGTT
41[98]	AAGGCCGTAAAATACGTAATGGCAAAA

29[119]	GGTTTCCACCGGAAACAATCGCTCTCA
25[182]	GACATTCCAATAGAAAATTCATATTACG
41[182]	CTGACCTGAAAGAGGACAGATATGCCCT
60[174]	GTCAATACGATGCTAGAATGCCAACGGC
2[9]	TAGCTTACCCCTGACGAAGCAAACCCCC
27[140]	CGGCACCTTCGCCATTCAAGGCCGACGTT
39[203]	TGAATTATCAGTGAATAAGGCGAGTAAT
27[98]	GACAGTAGCGGGCCTTCGCGCAAGGC
25[203]	GGGAAGGATAAGTTATTTGACGTAGA
23[182]	CCGGAAATTAGAGCCAGCAAAAAAGGGC
20[202]	CCACCAGGGAACCGCCTCCCTGTCAGAC
29[98]	GATTAAGCGTACAGGCCATGTTCTCC
33[98]	GCGGAATATAATGGAAGGGTTAACAGA
2[324]	ACCATAAATCAAAAACATAAAGAAAATTA
2[240]	CACTGCGGAATCGTGGATAATGGGGCGC
2[93]	AATACAAAGGCTATATTAATGGTAGCTCA
2[261]	CAGTATTCAATTGAATAGCCTTGCATCAATT
2[219]	AGAACTGGATAGCGTCTCATACCTGTTA
2[156]	GTTGAGAGGCTTTGAAAGGCTGATTCCA
2[30]	ATCAGTCAGAAGCAACTTCAATAATTGCTC
2[282]	CTCCAAATGCTTAATGTAATAAGCATTAA
2[303]	CACCAGAAAACGAGAACCAAATACAGGCAA
2[51]	AATTGCATCAAAAAGATATCGCTCATT
2[114]	AATATTGCCTGAGAGCAACCGTGCAACTAA
2[177]	CCAAAGTTTGCCAGTAAAGATTAGATTAA
64[223]	CACACGATGATAGCACCACCAAGCAGAAGTCA
5[87]	GAATATCCAATCCAATAAACACATGTTGTC
5[22]	TAGAGAAAATTAAATTGAGGCCAGTAAGTGT
5[169]	ATTCTGCAATAGTGTACGAGCATGTAGAATT

63[203]	TTTAATGCGCGAACCCAGTAAGTCAAAGTTGC
5[316]	GGCAAATAAGAATAATGCCATATTAACAGA
5[127]	AGTACGCCCTCGGCACAATAGATAAGTCCTAA
58[230]	ACGTGCCGGCGTTCCGCCGGCGCGGGCG
5[232]	GCTATACGCTATTAGAATTACCTTTTAATT
5[43]	CTTTGTTAGTTAATATAAAGTACCGACACCAA
1[144]	CAAGAGACTACCTTTAAGTGTCTGGTCAATAT
5[211]	CAAATGAATCCTTGAATTACATTAAACAAAAGA
1[60]	GTATTTCAAATATATTATAAGAGGGTTTAA
5[148]	TTCCATAAGGTCTGAGAAAAATAATATCCCCCTC
5[190]	GTTTGACTTAGATTACAATAATCGGGAAAACAAA
5[295]	CATCCAATTACTAGATCAACAGTAGGGCTTCCGC
5[64]	GCGGATGGAGAAAACAAGTAATTCTGTCCAGGTT
5[106]	ACATGTTAACTATATATGCAGAACCGCCTCGGT
1[186]	AATAGACGCTGAGAAGAGTCGAACCGAGTCAAAAG
1[249]	AAATGCTTCTGAAATCGTTTCATTAATT
5[253]	GAGCTGAAATAACCTCAGTACATAAATCAACGCG
1[39]	GAATTTCATCTTGTACCTGTACCTTAGCGAAC
1[102]	CTAGTAAATGCTGATGCAAATAATGCTCCGGAGA
1[228]	TTTATTAATTCCCTTAGGTCAATATAATTAA
1[333]	CCATAAATAAGGCGTTAAAGAATTAGCCTAAATC
1[81]	CGAGCAAGACAAAGAACCGCCTAGACGAAAGAC
1[291]	CGCAAAAGCCTTTAGTAATAGTAGTCTTGC
1[123]	TCATTAGGTTGGITATATTAAATATTCTAGCT
1[207]	ATTAAAACATAGCGATAGCCATTAGAAGTAATGT
22[202]	TGTAGCGAATGAAACCATCGACCGACTTGAGCCAT
1[165]	TAATAATTATCAAAATCATTAACAGTCGGAGACA
61[147]	CGTTGGCCGCACAGGCGGCCAGCCGAGGATTGCC
23[105]	GGATTAGCTGCCTATTGATCCTCATTAAAGCCA

34[195]	TGCGGGAGCCTAATAATGAAAACAGGGAAAGCGCA
1[312]	GAGAACACCGGAATCATAATAATCAAACATTAT
35[203]	CAAATCAAGAGCAACACTAAGTACCGCACGCCAA
59[98]	AGTTGAGAATTCCATGGTCCGGTCCACGCTGGTT
59[217]	GCTGGCAGCCTCCGTGAGGAAAACCGTCCACCAGT
43[203]	CGACCTGCTCCATGTCATAAGAGAACCGTGCTCAT
29[203]	GAAGCCCGCTAATATCAGAGAGATAACCAGTAGCTA
59[147]	GTGATGAGCGGCGGGCCTTTGGTGCTCATCCCT
40[195]	TTGCCCTAACTTAACGTTAAAGATTAGGAATAC
39[112]	AAAAAAAAGGCTCCATTGCGCCGACAATGGGGATCG
5[0]	AGCAATAACCGTGTGAACATGTAATTAGGCGGTT
2[202]	CAACTTAATAGTAAAATATGCCTGTACATTCTG
28[195]	AATAATATTAGCAATCACAATAACCGATTGAGGGA
57[126]	GCCTGTGCACTCTGTACCGTAATCATGGTCTTTA
1[18]	GCATTGGTTGAAATACCGAAGCAACAGGTAGGAT
62[121]	CTGGTATTGGCGCCAGGCCTGGCAAATCAAGTGTGTT
55[95]	TGGCACAACAAAGCATAAAGTGTATTAATGAGCGCGGG
58[114]	CAGGGGTACCGAGCTCGGTGAAATCCTTATCCTGAGA
55[221]	AAAGGTTATCATATCTGGTCAGTCGAACGACCTAAAA
60[128]	TGTAATTCGTCATACCGGGGGTTACTGCGCCAGCAAA
60[191]	ACTCAAACCGCTGGTCAGCAGCAGCTTACCTGCGGC
2[72]	GATAGGAAGCTTGAGAGATCTCATATGTACCCGACGA
63[147]	TCACCAAGTGAGATAACGCTGAGACGCTCACTGCCCTTCTT
34[139]	CAATATACAGATGAATATACAAACGGATTGCCGTGACGATCT
29[210]	TTTTAAAGAAGGATACATAACCACGGATAAAATTGACGGA
20[181]	CCGCCGACCGGAACCAAGAGCATCGGCATTCGGAGCAAGG
24[132]	TGTAAACTGCTCAGCGTATAACTGGTAAGATATTCAAAACA
38[153]	TGAATTGTCGTCAAACAATGTAACAGTTGCACCCAGCTAT
21[140]	TAACGGGGTCAGGCGCAGGTAGACGATTGGCCTTAAGTTT

63[161]	AGAATACGTGGCACTTCTGACGTTGGAGGGTAAACATCCCA
58[160]	AGCACATAGGGTAAAGTTAAAGATAATATGTTCCACTGAAAG
30[132]	ATAACCTCCAGTCATGCGCAATCCAGCCGGATTGCCAGCT
20[160]	GGTGAGCATCTTCATAATCCCCTTATTAGCGTCGAGAGG
20[118]	AATAAATGATACAGGAGTGTAAACAGTTAACCCCCGATTAGC
43[140]	CAAGCGCAAACAAGGCTTGGAACGAGAATTCTGGTTAT
41[168]	GGCGCATGAACGAGTAGTATTGAGGTGGTAGCAACGACCA
39[168]	GGCTTGAGGAACAAACATTAGTTAGTAAACAGCTGCTAATTG
63[182]	ATTTTGAAATGGCTTGGCCAATTAAAGATGTTGCCGGCTGGA
22[139]	CAGTGCCTACCAGGCGATAAGCAAATATTTAAATTTCATCA
43[98]	GAATACACTAAAACAAACGGGCTTGCACAACAAATCTCCA
20[97]	GAATGGAGCGTCATACATGGCTTCGGAACCTATTACTCCTC
23[161]	GTACCATTACCATTTCATAGCCAAATCCAGCATTGACAGGA
39[210]	CCTTATGGACGTTAACTAATCATACTAGATAGATAGAAGGCTT
37[168]	GGTAGAACGCAAGCCGTTTCATCGGGAGTTCCAGACTTACA
43[168]	TTGTATCGAACGGTGTACAGGCTACAGAAGTACAACGGAGAT
25[161]	CAGCGCCAAGACAATCACCAGTAGCTGATATAATCGAGTAA
24[195]	TTGGGAACGTCACCGTTTCCACCAACCACCAACCAGAG
34[223]	GCGAGGCCTTTAGATAAACACGATTTGGAGAATATTGAGC
27[161]	AAATTAAGACTCCTTATGGTTACCAACCCGTCGGTGCCGG
23[119]	GGGGTTGTTAATATTTGTTCTGGCCTCCTGTAACCGTAA
35[119]	TTCAGGTTGAATACCAAGTGCACAGCCCTCATAGTCAACTT
29[161]	AGTAAGAGCAAGAAAGAACTGGCATGACCAGGCAAAGTGCCA
5[274]	CTACTATCATATGCGTTATATATGTGAGTGAAAGGTGTATTCAA
63[105]	GAGAGGCAGCAAGCGAAATCGCGGCATCTCCAGCGCAGTGTCCCTGC
32[111]	TTAATTAGGGATAGGCAGAAATTGGGTAGATCGGTCGGCCTCAGGAAG
38[118]	CAACAGTTTCAGCGTCCACAGCCAATAGAAATTGCCTCTGATATCATC
57[196]	GGTGTCCGGTGCTGGTCCGTTTCGTCTTAGCTCCAACAAAGG
57[175]	CGCAACCAACCAGATTGCCGTTCCGAATAGATTCCACTACAGAGAT

24[223]	AATTATCACCGTCATAGCAGCCTTAGCCAGAGCCCACCCCTCAGAGCCG
37[126]	TAGCGTAATTGCTTTAACGTATCCTGACAGATGAAAATCCTAGAGACG
64[90]	TGCCCAATCCTGTCTGCAGCGGTCCCCCTGCATCTCGCGTCCTCAC
43[119]	TTTGACCCCCAGCGTTCATGCAGCAGCCCATAAGAAAGGAGTGCTAAA
35[168]	TCATCGTAAATCAAGCTAACGCAGCCAGCAGTTGGCGGTATGAATCT
28[153]	AGGCCAGCTTCTGATTCTCATGTGAGTGTATAAGTGCCGTTGCCTGAGTAA
Capture strands	Sequence (5'-3')
31[119]	AAAAAAA CGGAAAATTGCCGAACGTTAATATTCC
31[140]	AAAAAAA AGCGGATCGACAACACTCGTATTGGCAAT
31[161]	AAAAAAA TGCTCATTGCCGATAAGCCAATAACTTCAGAGAAATTTC
31[182]	AAAAAAA ACATAAAAATAGCAGCCTTAAGCGTCT
31[203]	AAAAAAA TTAGACGTTAACGTCAATTGCCAG
33[119]	AAAAAAA TGATTATTGTTGGATTATAGTAGATT
33[140]	AAAAAAA TCACAATTATCCAACAATTCAAACCTGTGGAGCGACGGCC
33[161]	AAAAAAA TACCAACGATTAGTTGCTATTACCTTTATATT
33[182]	AAAAAAA TTCCAGAGGTTTGAAGCCTTAGGAATC
33[203]	AAAAAAA TTACAAACGAACCTCCGACTTAGCAAG
56[118]	AAAAAAA TCGTTAAGCAAAATTGTTATCGGGTGCCTAATGAGAAC
56[139]	AAAAAAA TACACTGAAGAATATAGCTGTACTCACATTAATTG
56[160]	AAAAAAA TTGCTCGTGAGTGTAAAAAGCCAGCAGCAAATGAACAGTGCC
56[181]	AAAAAAA TGGTAATACAAGAGTAGAGCCAAGCATCACCTGCCAGTATT
56[202]	AAAAAAA GGGTCACACGTGGAGAGCACTCAAATATCAAACCCATAAAC
64[118]	AAAAAAA GAGTTCGGTTGCTCGTGCAGCTGCAAAGCCTGCGCTACGATC
64[139]	AAAAAAA CTTCACCGGTGGTGCTTCCAGTCGGGTGAGCTATTCC
64[160]	AAAAAAA CGCGGGCAACAGCTATAGGGTCAAAAGCGG
64[181]	AAAAAAA AGAACCCAGACAATAACACCGCCTGAAAAATCTA
64[202]	AAAAAAA GACATT CATTAGTCAGAGGTGAGGCAGGTGAACCTAAC
Footholds	Sequence (5'-3')
4[5] fh _{3'}	TCTGAATGCTGGATCTC TCAGAGTCAGGTTACCGCCACCCCTCAACG

4[26] fh _{4'}	TCTGAATGC GACTCTAA AGACCGTATTATAACGTACTCAGGAAGAG
4[47] fh _{5'}	TCTGAATGC GACGAGTT TTGAGAGCGAACGCCCGAATAGTAAGA
4[68] fh _{6'}	TCTGAATGC GGTCTAAT TTCAAATTAAGAACATCAGAAAAGCCAAAG
4[89] fh _{7'}	TCTGAATGC TAGAAGTC GGGTAGCTTCGCTTAATTGCT
4[110] fh _{8'}	TCTGAATGC AATAGTCC GATAACAGGTCCGTAAAAGTAGCATCAG
4[131] fh ₁	TCTGAATGC GAACTGGT GATATTCTGGAGCAAAAAACCAAATCACCAAAGTTCA
4[152] fh ₂	TCTGAATGC ACGCAAGG GTCAAAATAGCTACCAGACGACGATGAA
4[173] fh ₃	TCTGAATGC TGGATCTC GGTGAGCAAAAGAGAACGGTATTCATCC
4[194] fh ₄	TCTGAATGC GACTCTAA GTAGGAGGGGGTCTTCCTTATCAACC
4[215] fh ₅	TCTGAATGC CACGAGTT ATGCAGTTAGTGATGAAACAAACAT
4[236] fh ₆	TCTGAATGC GGTCTAAT AGAACCCCAATAATTACCTGAGCAATTCA
4[257] fh ₇	TCTGAATGC TAGAAGTC CGAACACATAAAAGCGAATTATTATGG
4[278] fh ₈	TCTGAATGC AATAGTCC GGGAGACCCCTATTCAGGAAATTACAA
4[299] fh _{1'}	TCTGAATGC GAACTGGT GACCCACAGTCCTCAGAGCCACCCAA
4[320] fh _{2'}	TCTGAATGC ACGCAAGG GGTTGTATGACCGCCACCTCAGAAAATT
Feet	Sequence (5'-3')
59[109]F1N	GCATTCAAGATT CCCCACCGCGTGCCTGTTAGACGAAGATGCCGGTTACTTGA
61[213]F2N	GCATTCAAGATT ATCATAAAATATCTCGTCTAGAACGTCAGCGTAGCATCAATGAGCC
Blocking strands	Sequence (5'-3')
B ₁	ACCAGTTCGCATTCTCTAGCTTACT
B ₂	CCTTGCCTGCATTCTCTCCTTATCG
B ₃	GAGATCCA GCATTCT TTTGTACGAAC
B ₄	TTAGAGTC GCATTCT TATTAGCAACG
B ₅	AACTCGTC GCATTCT TCTCACTAATT
B ₆	ATTAGACC GCATTCT TTTGAGTTCCG
B ₇	GACTTCTA GCATTCT TTTCACCTTCA
B ₈	GGACTATT GCATTCT GTTGTAGATCC
Removal strands	Sequence (5'-3')
R ₁	AGTAAGCTAGAGAATGCGAACTGGT

R ₂	CGATAAGGAGAGAATGCACGCAAGG
R ₃	GTTCGTACAAA GAATGCTGGATCTC
R ₄	CGTTGCTAATA GAATGC GA CTCTAA
R ₅	AATTAGTGAGA GAATGC GACGAGTT
R ₆	CGGAACTCAA GAATGC GG TCTAAT
R ₇	TGAAAGTGAAG GAATGCT AGAAGTC
R ₈	GGATCTACAAC GAATGC AATAGTCC

Supplementary Table 2 | Additions of blocking and removal strands for a full-turn clockwise rotation. All the fuel strands have a concentration of 250 μ M. So do those in Supplementary Table 3 and 4.

Steps	Strands added	Steps	Strands added
1 → 2	0.4 μ L B ₁ and 0.4 μ L R ₂	1' → 2'	1.2 μ L B ₁ and 0.8 μ L R ₂
2 → 3	0.8 μ L B ₂ and 0.4 μ L R ₃	2' → 3'	1.2 μ L B ₂ and 0.8 μ L R ₃
3 → 4	0.8 μ L B ₃ and 0.4 μ L R ₄	3' → 4'	1.2 μ L B ₃ and 0.8 μ L R ₄
4 → 5	0.8 μ L B ₄ and 0.4 μ L R ₅	4' → 5'	1.2 μ L B ₄ and 0.8 μ L R ₅
5 → 6	0.8 μ L B ₅ and 0.4 μ L R ₆	5' → 6'	1.2 μ L B ₅ and 0.8 μ L R ₆
6 → 7	0.8 μ L B ₆ and 0.4 μ L R ₇	6' → 7'	1.2 μ L B ₆ and 0.8 μ L R ₇
7 → 8	0.8 μ L B ₇ and 0.4 μ L R ₈	7' → 8'	1.2 μ L B ₇ and 0.8 μ L R ₈
8 → 1'	0.8 μ L B ₈ and 0.8 μ L R ₁	8' → 1	1.2 μ L B ₈ and 1.2 μ L R ₁

Supplementary Table 3 | Additions of blocking and removal strands for the plasmonic nanoclock from position 5-5' to position 5'-5 during the time-course CD measurements.

Steps	Strands added
5 → 6	0.4 μ L B ₅ and 0.4 μ L R ₆
6 → 7	0.8 μ L B ₆ and 0.4 μ L R ₇
7 → 8	0.8 μ L B ₇ and 0.4 μ L R ₈
8 → 1'	0.8 μ L B ₈ and 0.4 μ L R ₁
1' → 2'	0.8 μ L B ₁ and 0.4 μ L R ₂
2' → 3'	0.8 μ L B ₂ and 0.4 μ L R ₃
3' → 4'	0.8 μ L B ₃ and 0.4 μ L R ₄
4' → 5'	0.8 μ L B ₄ and 0.8 μ L R ₅

Supplementary Table 4 | Additions of blocking and removal strands for a 15-step counterclockwise rotation followed by a 9-step clockwise rotation.

Counterclockwise Steps	Strands added	Clockwise Steps	Strands added
1 → 8'	0.4 μL B ₁ and 0.4 μL R ₈	2 → 3	1.2 μL B ₂ and 1.6 μL R ₃
8' → 7'	0.8 μL B ₈ and 0.4 μL R ₇	3 → 4	2 μL B ₃ and 1.6 μL R ₄
7' → 6'	0.8 μL B ₇ and 0.4 μL R ₆	4 → 5	2 μL B ₄ and 1.6 μL R ₅
6' → 5'	0.8 μL B ₆ and 0.4 μL R ₅	5 → 6	2 μL B ₅ and 1.6 μL R ₆
5' → 4'	0.8 μL B ₅ and 0.4 μL R ₄	6 → 7	2 μL B ₆ and 1.6 μL R ₇
4' → 3'	0.8 μL B ₄ and 0.4 μL R ₃	7 → 8	2 μL B ₇ and 1.6 μL R ₈
3' → 2'	0.8 μL B ₃ and 0.4 μL R ₂	8 → 1'	2 μL B ₈ and 1.6 μL R ₁
2' → 1'	0.8 μL B ₂ and 0.8 μL R ₁	1' → 2'	2 μL B ₁ and 1.6 μL R ₂
1' → 8	1.2 μL B ₁ and 0.8 μL R ₈	2' → 3'	2 μL B ₂ and 2.4 μL R ₃
8 → 7	1.2 μL B ₈ and 0.8 μL R ₇		
7 → 6	1.2 μL B ₇ and 0.8 μL R ₆		
6 → 5	1.2 μL B ₆ and 0.8 μL R ₅		
5 → 4	1.2 μL B ₅ and 0.8 μL R ₄		
4 → 3	1.2 μL B ₄ and 0.8 μL R ₃		
3 → 2	1.2 μL B ₃ and 0.8 μL R ₂		

Supplementary Table 5 | Track arrangements of the autonomous plasmonic nanoclocks for clockwise rotation.

	Locking strands	Substrates
Position 1–2	fh ₁ and fh _{1'}	@ fh ₂ and fh _{2'}
Position 1–2–3	fh ₁ and fh _{1'}	@ fh ₂ –fh ₃ and fh _{2'} –fh _{3'}
Position 1–2–3–4	fh ₁ and fh _{1'}	@ fh ₂ –fh ₄ and fh _{2'} –fh _{4'}
Position 1–2–3–4–5	fh ₁ and fh _{1'}	@ fh ₂ –fh ₅ and fh _{2'} –fh _{5'}
Position 1–2–3–4–5–6	fh ₁ and fh _{1'}	@ fh ₂ –fh ₆ and fh _{2'} –fh _{6'}
Position 1–2–3–4–5–6–7	fh ₁ and fh _{1'}	@ fh ₂ –fh ₇ and fh _{2'} –fh _{7'}

Supplementary Table 6 | Track arrangements of the autonomous plasmonic nanoclocks with open sites.

	Locking strands	Substrates
Position 1–2–3–x–5	fh ₁ and fh _{1'}	@ fh ₂ –fh ₃ , fh ₅ and fh _{2'} –fh _{3'} , fh _{5'}
Position 1–2–x–x–5	fh ₁ and fh _{1'}	@ fh ₂ , fh ₅ and fh _{2'} , fh _{5'}

Supplementary Table 7 | Track arrangements of the autonomous plasmonic nanoclocks for counterclockwise rotation.

	Locking strands	Substrates
Position 1–8'	fh ₁ and fh _{1'}	@ fh ₈ and fh _{8'}
Position 1–8'–7'	fh ₁ and fh _{1'}	@ fh ₈ –fh ₇ and fh _{8'} –fh _{7'}
Position 1–8'–7'–6'	fh ₁ and fh _{1'}	@ fh ₈ –fh ₆ and fh _{8'} –fh _{6'}
Position 1–8'–7'–6'–5'	fh ₁ and fh _{1'}	@ fh ₈ –fh ₅ and fh _{8'} –fh _{5'}
Position 1–8'–7'–6'–5'–4'	fh ₁ and fh _{1'}	@ fh ₈ –fh ₄ and fh _{8'} –fh _{4'}
Position 1–8'–7'–6'–5'–4'–3'	fh ₁ and fh _{1'}	@ fh ₈ –fh ₃ and fh _{8'} –fh _{3'}

Supplementary Table 8 | Sequences of the functional strands for autonomous rotation.

Substrate_footholds	Sequence (5'-3')
4[5] Sub _{3'}	GAGTTGG rA TAGGTTATGAGATTGTT TCAGAGTCAGGTTACGCCACCCCTCAACG
4[26] Sub _{4'}	GAGTTGG rA TAGGTTATGAGATTGTT AGACCGTATTATACCGTACTCAGGAAGAG
4[47] Sub _{5'}	GAGTTGG rA TAGGTTATGAGATTGTT TTGAGAGCGGAACGCCCGGAATAGTAAGA
4[68] Sub _{6'}	GAGTTGG rA TAGGTTATGAGATTGTT TTCAAATTAAGAACATGAAAAGCCAAAG
4[89] Sub _{7'}	GAGTTGG rA TAGGTTATGAGATTGTT GGGTAGCTATTGCTTAATTGCT
4[110] Sub _{8'}	GAGTTGG rA TAGGTTATGAGATTGTT GATAACAGGTCCGTAAAAGCATCAG
4[152] Sub ₂	GAGTTGG rA TAGGTTATGAGATTGTT GTCAAAATAGCTACCAGACGACGATGAA
4[173] Sub ₃	GAGTTGG rA TAGGTTATGAGATTGTT GGTGAGCAAAAGAGAACGGTATTCATCC
4[194] Sub ₄	GAGTTGG rA TAGGTTATGAGATTGTT GTAGGAGGGGGCTTCTTATCAACC
4[215] Sub ₅	GAGTTGG rA TAGGTTATGAGATTGTT ATGCAGTTAGTGATGAAACAAACAT
4[236] Sub ₆	GAGTTGG rA TAGGTTATGAGATTGTT AGAACCCCAATAATTACCTGAGCAATTCA
4[257] Sub ₇	GAGTTGG rA TAGGTTATGAGATTGTT CGCACACATAAAAGGCGAATTATTATGG
4[278] Sub ₈	GAGTTGG rA TAGGTTATGAGATTGTT GGGAGACCCCTATTCAGGAAATTACAA
4[320] Sub _{2'}	GAGTTGG rA TAGGTTATGAGATTGTT GGTTGTATGACCGCCACCCCTCAGAAAATT
DNAzyme_feet	Sequence (5'-3')
59[109]	CATAACCTA CCGAGCCGGTCGAATCAACTC TCTT CCCCACCGCGTGCCTGTTCAGACGAAGATGCC
61[213]	CATAACCTA CCGAGCCGGTCGAATCAACTC TCTT ATCATAAAATATCTCGTCTAGAACGTCAGCGTAGC
58[114]locking2	GCATTCAGATT CAGGGTACCGAGCTCGGTGAAATCCCTATCCTGAGA
62[206]locking1	GCATTCAGATT AAACTTAATGCGCGAACCCAGTAAGTCAAAGTTGC
Removal strand r	GTATCTGTCGT ACCTACCGAGCCGGTCGAA
Blocking strand b	TTGATTGACCGGCTCGGTAGGT ACGACAGATAC
Revised staples	Sequence (5'-3')
56[97]	GGGTTACTTGATGGCACAAACAAAGCATAAAGTGTATTAATGAGCGCGGG
57[206]	ATCAATGAGCCGGGTACACGTGGAGAGCACTCAAATATCAAACCCATA
56[212]	AAAAAAA GGTGCGGGGTATTGCAGGACTTG

Supplementary Table 9 | Additions of the trigger strands to actuate the autonomous plasmonic nanoclocks.

Steps	Strands added
1	100 μM 1 μL removal strand r
2	250 μM 0.5 μL B_1